



PCT

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/009,792A

DATE: 04/03/2003  
TIME: 14:26:35

Input Set : A:\HYLEE60.001.TXT  
Output Set: N:\CRF4\04032003\J009792A.raw

4 <110> APPLICANT: LEE, Sang-Yup  
5 JEONG, Ki-Jun  
7 <120> TITLE OF INVENTION: ESCHERICHIA COLI STRAIN SECRETING HUMAN  
8 GRANULOCYTE COLONY STIMULATING FACTOR (G-CSF)  
11 <130> FILE REFERENCE: HYLEE60.001APC  
13 <140> CURRENT APPLICATION NUMBER: US 10/009,792A  
**C--> 14 <141> CURRENT FILING DATE: 2002-10-29**  
16 <150> PRIOR APPLICATION NUMBER: PCT/KR01/00549  
17 <151> PRIOR FILING DATE: 2001-03-31  
19 <150> PRIOR APPLICATION NUMBER: KR 10-2000-0017052  
20 <151> PRIOR FILING DATE: 2000-03-31  
22 <160> NUMBER OF SEQ ID NOS: 27  
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
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27 <211> LENGTH: 13  
28 <212> TYPE: PRT  
29 <213> ORGANISM: Artificial Sequence  
31 <220> FEATURE:  
32 <223> OTHER INFORMATION: Oligopeptide  
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37 1 5 10  
40 <210> SEQ ID NO: 2  
41 <211> LENGTH: 29  
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43 <213> ORGANISM: Artificial Sequence  
45 <220> FEATURE:  
46 <223> OTHER INFORMATION: Primer  
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52 <211> LENGTH: 32  
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54 <213> ORGANISM: Artificial Sequence  
56 <220> FEATURE:  
57 <223> OTHER INFORMATION: Primer  
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62 <210> SEQ ID NO: 4  
63 <211> LENGTH: 50  
64 <212> TYPE: DNA  
65 <213> ORGANISM: Artificial Sequence  
67 <220> FEATURE:

ENTERED

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68 <223> OTHER INFORMATION: Primer  
70 <400> SEQUENCE: 4  
71 tcttcgggtt agcacatgtt gttagtgcca cacaqcttctt cttggaaagc 50  
73 <210> SEQ ID NO: 5  
74 <211> LENGTH: 50  
75 <212> TYPE: DNA  
76 <213> ORGANISM: Artificial Sequence  
78 <220> FEATURE:  
79 <223> OTHER INFORMATION: Primer  
81 <400> SEQUENCE: 5  
82 gctgtgcaccccgaggcgt tggtgttgtt cggacactct ctgggcatcc 50  
84 <210> SEQ ID NO: 6  
85 <211> LENGTH: 50  
86 <212> TYPE: DNA  
87 <213> ORGANISM: Artificial Sequence  
89 <220> FEATURE:  
90 <223> OTHER INFORMATION: Primer  
92 <400> SEQUENCE: 6  
93 ctggctqqqq cagctgtca qgggatgccca gggatgcc agagagtgtc 50  
95 <210> SEQ ID NO: 7  
96 <211> LENGTH: 48  
97 <212> TYPE: DNA  
98 <213> ORGANISM: Artificial Sequence  
100 <220> FEATURE:  
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106 <210> SEQ ID NO: 8  
107 <211> LENGTH: 32  
108 <212> TYPE: DNA  
109 <213> ORGANISM: Artificial Sequence  
111 <220> FEATURE:  
112 <223> OTHER INFORMATION: Primer  
114 <400> SEQUENCE: 8  
115 gaattccatat gaccccccgtt ggccctgtcc gc 32  
117 <210> SEQ ID NO: 9  
118 <211> LENGTH: 32  
119 <212> TYPE: DNA  
120 <213> ORGANISM: Artificial Sequence  
122 <220> FEATURE:  
123 <223> OTHER INFORMATION: Primer  
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128 <210> SEQ ID NO: 10  
129 <211> LENGTH: 33  
130 <212> TYPE: DNA  
131 <213> ORGANISM: Artificial Sequence  
133 <220> FEATURE:  
134 <223> OTHER INFORMATION: Primer

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136 <400> SEQUENCE: 10  
137 qqaattcaca tqttaaagt taaaaaagaaa tt  
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140 <211> LENGTH: 29  
141 <212> TYPE: DNA  
142 <213> ORGANISM: Artificial Sequence  
144 <220> FEATURE:  
145 <223> OTHER INFORMATION: Primer  
147 <400> SEQUENCE: 11  
148 ggctggacct aacggagttg cagaggcg 29  
150 <210> SEQ ID NO: 12  
151 <211> LENGTH: 33  
152 <212> TYPE: DNA  
153 <213> ORGANISM: Artificial Sequence  
155 <220> FEATURE:  
156 <223> OTHER INFORMATION: Primer  
158 <400> SEQUENCE: 12  
159 gcaaccgcct ctqcaactcc gttaggicca gcc 33  
161 <210> SEQ ID NO: 13  
162 <211> LENGTH: 33  
163 <212> TYPE: DNA  
164 <213> ORGANISM: Artificial Sequence  
166 <220> FEATURE:  
167 <223> OTHER INFORMATION: Primer  
169 <400> SEQUENCE: 13  
170 gcgaattctt taaagccacg ttgtgtcctc aaa 33  
172 <210> SEQ ID NO: 14  
173 <211> LENGTH: 36  
174 <212> TYPE: DNA  
175 <213> ORGANISM: Artificial Sequence  
177 <220> FEATURE:  
178 <223> OTHER INFORMATION: Primer  
180 <400> SEQUENCE: 14  
181 gcgaattctt taaattagaa aaactcatcg agcata 36  
183 <210> SEQ ID NO: 15  
184 <211> LENGTH: 39  
185 <212> TYPE: DNA  
186 <213> ORGANISM: Artificial Sequence  
188 <220> FEATURE:  
189 <223> OTHER INFORMATION: Primer  
191 <400> SEQUENCE: 15  
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194 <210> SEQ ID NO: 16  
195 <211> LENGTH: 41  
196 <212> TYPE: DNA  
197 <213> ORGANISM: Artificial Sequence  
199 <220> FEATURE:  
200 <223> OTHER INFORMATION: Primer  
202 <400> SEQUENCE: 16

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203 gatatggta tggtagtgtt gggcccaac tgcagaggcg q 41  
205 <210> SEQ ID NO: 17  
206 <211> LENGTH: 507  
207 <212> TYPE: DNA  
208 <213> ORGANISM: Homo sapiens  
210 <400> SEQUENCE: 17  
211 atggctggac ctgecaccca gagccccatg aagctgtgg ccctgcagct gctgcgtgg 60  
212 agtgcactt ggacagtgc a ggaagccacc cccctggcc ctgcgcagtc cctgccccag 120  
213 agtttcgtgc tcaagtgtt agagcaagtg agaaagatcc agggcgatgg cgccgcgtc 180  
214 caggagaacg tggeaggctg cttgagccaa ctccatagcg gctttctt ctaccagggg 240  
215 ctccgtcagg ccctggaaagg gatctccccc gatgtggtc ccacatttgcg aacactgcag 300  
216 ctggacgtcg ccgactttgc caccaccate tggeagcaga tggaaaact gggatggcc 360  
217 cctgccttcg a gcccaccca gggggccatg ccqgcttcg cctctgttt ccagcgcgg 420  
218 gcaggagggg tcctaqtgc ctccccatcg cagaatccc tggaggtgtc gtaaccgcgtt 480  
219 ctacggccacc ttgcggcagcc aataaa 507  
221 <210> SEQ ID NO: 18  
222 <211> LENGTH: 615  
223 <212> TYPE: DNA  
224 <213> ORGANISM: Homo sapiens  
226 <400> SEQUENCE: 18  
227 atggctggac ctgcaccca gagccccatg aagctgtgg ccctgcagct gctgcgtgg 60  
228 agtgcactt ggacagtgc a ggaagccacc cccctggcc ctgcgcagtc cctgccccag 120  
229 agtttcgtgc tcaagtgtt agagcaagtg agaaagatcc agggcgatgg cgccgcgtc 180  
230 caggagaacg tttgtggccac ctacaagctg tgccaccccg aggagctgtt gctgctcg 240  
231 cactctctgg gcatccccctg ggtccccctg agcagctgcc ccagccagcc cctgcagctg 300  
232 gcaggctgt ttagccact ccatacgccg cttttctt accaggggct cctgcaggcc 360  
233 ctggagggta tttccccctg gttgggtccc acctggaca cactgcagct ggacqtcg 420  
234 gactttgcca ccaccatctg qcagcagatg qaaqaactgg qaatggccc tggccctgcag 480  
235 cccacccagg gtgcattgc qcccttcgccc tctgtttcc aqgcggggc aggaggggtc 540  
236 ctatgtcct cccatctgc a gagtttctg gaggtgtcgt accgcgttct aqgcacatt 600  
237 gcccagccct aataaa 615  
239 <210> SEQ ID NO: 19  
240 <211> LENGTH: 174  
241 <212> TYPE: PRT  
242 <213> ORGANISM: Homo sapiens  
244 <400> SEQUENCE: 19  
245 Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys  
246 1 5 10 15  
247 Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln  
248 20 25 30  
249 Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val  
250 35 40 45  
251 Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys  
252 50 55 60  
253 Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser  
254 65 70 75 80  
255 Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser  
256 85 90 95  
257 Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp

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258 100 105 110  
259 Phe Ala Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro  
260 115 120 125  
261 Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe  
262 130 135 140  
263 Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe  
264 145 150 155 160  
265 Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro  
266 165 170  
269 <210> SEQ ID NO: 20  
270 <211> LENGTH: 531  
271 <212> TYPE: DNA  
272 <213> ORGANISM: Homo sapiens  
274 <400> SEQUENCE: 20  
275 atgacccccc tggccctgc cagtcctcg cccccagact tcctgttcaa gtgcttagag 60  
276 caaigagga agatccaggc cgatggcgca ggcgtcccaqg agaagctqtg tgccacccatc 120  
277 aagctgtgee acccccgagga gctgggtgtg ctccggacact ctctggcat cccctggct 180  
278 cccctggaca qctggccctg ccaggccctg cagtcggcag gctgcttqag ccaactccat 240  
279 agcggcctt tcctctacca ggggttcctg caggccctgg aagggtatctc ccccgagttg 300  
280 ggtcccacct tggacacact gcaagctggac gtgcggcact ttgccaccac catctggcag 360  
281 cagatggaaq aactgggaat ggcctctgcc ctgcageccca cccagggtgc catqccggcc 420  
282 ttcgcctctg ctttccagcg ccgggcaggc ggggtcttag ttgcctccca tctgcagagc 480  
283 ttcctggagg tgcgttaccg ctttctacgc cacctgtcccc agccctaata a 531  
285 <210> SEQ ID NO: 21  
286 <211> LENGTH: 175  
287 <212> TYPE: PRT  
288 <213> ORGANISM: Homo sapiens  
290 <400> SEQUENCE: 21  
291 Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu  
292 1 5 10 15  
293 Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu  
294 20 25 30  
295 Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu  
296 35 40 45  
297 Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser  
298 50 55 60  
299 Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His  
300 65 70 75 80  
301 Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile  
302 85 90 95  
303 Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala  
304 100 105 110  
305 Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala  
306 115 120 125  
307 Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala  
308 130 135 140  
309 Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser  
310 145 150 155 160  
311 Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro

**VERIFICATION SUMMARY**

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DATE: 04/03/2003

TIME: 14:26:36

Input Set : A:\HYLEE60.001.TXT

Output Set: N:\CRF4\04032003\J009792A.raw

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date